

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 18, 2001, 15:56:47 ; Search time 19.26 Seconds

(without alignments)
3021.670 Million cell updates/sec

Title: US-09-587-111-5

Perfect score: 4004
Sequence: 1 MTPSSSPVFRLTLDDGQE.....EDEDGASENVVPVQLQSN 764Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR:68:***
2: PIR:1:***
3: PIR:3:***
4: PIR:4:***

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1652	41.3	838	2 T09054	capsaicin receptor
2	634	15.8	725	3 JC7531	calcium transport
3	414	10.3	900	2 T33026	hypothetical prote
4	392.5	9.8	790	2 T20312	hypothetical prote
5	364	9.1	937	2 T37241	olfactory channel
6	261	6.5	519	2 T24772	hypothetical prote
7	209	5.2	1188	2 T19552	hypothetical prote
8	197.5	4.9	1124	2 JH0588	calmodulin-binding
9	191	4.8	1274	2 JN0015	trp protein - frui
10	190.5	4.8	1275	2 JU0092	trp protein - frui
11	174	4.3	810	2 T38361	TRPC1 protein - hu
12	167.5	4.2	934	1 H71274	probable ankyrin - hu
13	157.5	3.9	481	2 T23729	hypothetical prote
14	157	3.9	1549	2 T13940	ankyrin - fruit fl
15	151	3.8	1765	2 T42714	ankyrin 3, splice
16	151	3.8	1940	2 T42715	ankyrin 3, splice
17	151	3.8	1943	2 T42713	ankyrin 3, splice
18	151	3.8	1961	2 T42716	ankyrin 3, splice
19	151	3.8	3924	2 S37431	ankyrin 2, neurona
20	150.5	3.8	793	2 S68238	trp-1 protein - hu
21	150	3.7	887	2 T03939	potassium channel
22	150	3.7	4377	2 A55575	ankyrin 3, long sp
23	147	3.7	1001	2 S30385	G9a protein - huma
24	143	3.6	842	2 T32258	hypothetical prote
25	141.5	3.5	683	2 A85044	hypothetical prote
26	140	3.5	1848	2 S37771	ankyrin, erythrocy
27	140	3.5	1862	2 T49502	ankyrin - mouse
28	139.5	3.5	1411	2 S30355	alpha-latroinsecto
29	138	3.4	1856	2 B35049	ankyrin 1, erythro

30	138	3.4	1880	2 A35049	ankyrin 1, erythro
31	138	3.4	1881	1 SJHUK	ankyrin 1, erythro
32	136	3.4	2352	2 T30201	Notch homolog prot
33	135	3.4	828	2 JC5807	trp3 protein - rat
34	134.5	3.4	1401	2 S11527	alpha-latrotoxin p
35	134.5	3.4	1435	2 T32930	hypothetical prote
36	133.5	3.3	642	2 S58154	hypothetical prote
37	133.5	3.3	1786	2 A57282	ankyrin-related pr
38	133.5	3.3	1815	2 T15346	elegans ankyrin-re
39	133.5	3.3	1867	2 T15344	ankyrin-related un
40	133.5	3.3	2039	2 T15347	ankyrin-related un
41	132	3.3	616	2 T00884	hypothetical prote
42	132	3.3	1184	2 T00253	gene Anknkn protei
43	132	3.3	1398	2 T21884	hypothetical prote
44	132	3.3	1964	2 T09059	notch4 - mouse
45	131.5	3.3	598	2 D71127	hypothetical prote

ALIGNMENTS

RESULT 1

capsaicin receptor - rat
N:Alternate names: vanilloid receptor subtype 1
C:Species: Rattus norvegicus (Norway rat)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C:Accession: T09054
R:Caterina, M.J.; Schumacher, M.A.; Tomlinage, M.; Rosen, T.A.; Levine, J.D.; Julius, Nature 389, 816-824, 1997
A:Title: The capsaicin receptor: A heat-activated ion channel in the pain pathway.
A:Reference number: Z16539; MUID:98007969
A:Accession: T09054
A>Status: preliminary; translated from CB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1838 <CAT>
A:Cross-references: EMBL:AF029310; MID:g2570932; PIDN:AAC53398.1; PID:g2570933
A:Experimental source: dorsal root ganglion
C:Keywords: ion channel; receptor

Query Match	41.38;	Score 1652;	DB 2;	Length 838;
Best Local Similarity	46.38;	Pred. No. 4.4e-120;		
Matches 359;	Conservative 127;	Mismatches 230;	Indels 60;	Gaps 15;
Db	18	GOEKGSEADRKGLDFGSLPMEQFQEDKRFAPQIRVN---	LNRYKRGTC-----	65
Qy	51	GKGDSEAS-----	PLDCPYEKGGLASCPILTVSSVLTIOKRGDPAASVPSQ	99
Db	66	---ASQPDNRFDRDLFNFAVSGVPEDLAFLPEYLSKTSKYLTDESEYTGSTGTCIM		121
Qy	100	DSVAGKRPRLRYRSTFDFVAVASQNCQELSLPFLQSRKRLTDESEFDPKGTCLL		159
Db	122	KAVLNLDGVNACILPLLDIDRDSGNPQPLVNAOCTDDYVRGSHALIAIEKRSLOCVKL		181
Qy	160	KAMLNHNQNDITALLLDVARKFDSLKQFVNAAGTSPYVGGQALHAIERRNNLTVTLL		219
Db	182	LVENGAVVHARACGRFQKGG--TCFYEGLPLSLACTOMDVSVLLEPHQPAISQA		240
Qy	220	LVENGADVQAANAGDFKRTKRGPEYFEGELPSLACTNOLATVKKLLQNSWCPAIDISA		279
Db	241	TDSGNTVLHVLWISNSAENIALVTSMYGDLLQAGARLCPTVQLBDIRMLQDLPKL		300
Qy	280	RDSVGNVHLALVEAVANTVDNTKFEVSMWNEILLAKKLHPTLKEITNRKCLTFLAL		339
Db	301	AAKSGKIGVLAIIQREIHREPECHRLSRKFTFMAVYGVHSLYDLSICIDCEKNSVLEVI		358
Qy	340	AF-HCKSPHRRMVVLEPLNKLLOAKMDLLPK-FEINPLCNLYMFLPAVAVHOPTLK		416
Db	400	AYSSSETPNRHMDLVEPLNKLLODKMDRVRKRIEYFNVFYCYCKMILTFPAAYRPV--		457

OY	417	KQAA- HLKK EVGSM LL TH LL LL LL GGIY LL V LL Q LL W LL PM RR HHV LL WIS PL DS FE LL	474
Db	458	-EGLP PL Y LL KL NT NG VD ERY TE GI LL SV SG V Y FF RG IO Y FL Q RR PS LS LL VD ST SEL LE	516
OY	475	LE Q ALL Y V SV Q VL CE FL A EW Y LL PL LL VS AL V GL W LL LY Y RG FO HT GI Y SV MI Q RV LL RD	534
Db	517	FV OS LE FM Y VL VE FS Q RE Y VS AW VF SL AG WT ML Y TR GF OO MG Y PA VI AE IK ML RD	576
OY	535	LL RF LL Y LV Y LF EG AV AL VS LS OE AM RP EA PT GN AT ES VP MG Q DE NGA-----	588
Db	577	LC RE ME Y VL VE LF EG ST AV LL IED -----G KN ---NS LP HE ST PH K RG S ACK GN	625
OY	589	OY RG LE NS LE LF KT IO MG EL A FO Q HL RG W LL LY LL AV LL Y LL NL ML AL MS ET	648
Db	626	SY NS Y ST CE LE F KT IO MG DL EF EN YD FA VF LL LA V IL LY ILL ML AL MS ET	685
OY	649	V NS V AT DS MS IM L OK AL SV LE MG Y W MC -R K RO AG VM LV Y G K PG SP DE RC FE VE	707
Db	666	V NK IM Q ES KN IM Q OR AT IL LD TE KS PL CK MR KA FR SK LL Q Y GT TP CK ND Y RC FE VD	745
OY	708	EY N MA SM Q TL PL IC ED PS GA-GV PR LE NP V LA SP KE DE D GA SE EN Y VP Q LL Q	762
Db	746	EY N MT MT NT NG IL IN ED GC NE GV RT LS FR SG ---RV SG RM KA FP AL PL LR	797

RESULT 2
JC7531
calcium transport protein, Cat1 - human
C:Species: Homo sapiens (man)
C:Date: 31-Mar-2001 #sequence_revision 31-Mar-2001 #text_change 31-Mar-2001
C:Accession: JC7531
R:Peng, J.B.; Chen, X.; Berger, U.V.; Wieremowicz, S.; Morton, C.C.; Vassiliev, P.M.; Brown, J.H.; Bredt, D.S. *Proc. Natl. Acad. Sci. USA* 98:1152-1156 (2001)
A:Title: Human calcium transport protein Cat1.
A:Reference number: JC7531; MUID:20551480
A:Accession: JC7531
A:Molecule type: mRNA
A:Residues: 1-725 <PDB>
A:Cross-references: GB:AF304463
C:Comment: This protein, a member of a family of Ca2+ channels, has a role in cellular calcium homeostasis in the endoplasmic reticulum, the Golgi apparatus, the plasma membrane, the
line and kidney.
C:Genetics:
A:Gene: Cat1
A:Map position: 7q33-34
A:Keywords: calcium channel; calcium transport; intestine; kidney; transport protein; trachea

[illegible]

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Db      331  MGAATYLLYITICFMCCLYRKLKRTNNRSPRDNLTLOQKLLQGEAYMMPKXIDRLUGEL 390
Qy      438  LILGGYLLVWGOLMYMRHHV--FTWISFTDSTFEILLFQALLTVTSQVLCFLAIEMY 495
Db      391  YVYIAITLITLVEVPDIFERRGVTFHFQQTLLGGPRFHVLLITVAFVWLIVMYRKLISAGE 450
Qy      496  LPLTASALVGLMNLILYYTRGFQHTGYISVNIQVLLRDLRFLLYLTVFRCFPAVALVS 555
Db      451  VYPMSEFALVDQNCVMYMFANGFQGLGPFITIMDKMIFGDLMRCKWMLNAVILIGFSAFYI 510
Qy      556  LSGEAMRPEADPTGNATVESQVPMGEQDEBSCAQYKGLBASLFLFKPTIGMCELAFQEQ 615
Db      511  IFQ-----TEDPELGHFYDYPALFSTPELR-LTIIDGPRANYVD 550
Qy      616  LHFRCGVNLLLVLLVLTYYLLMLLALMSETVNSAVTSMISWYLOKAIISYLEMENGY 675
Db      551  LPF--MYSITYAAARAITATLMLNLLRLAMNGDTHMYRAHNRDEIMRAQIVATVYMIERL 608
Qy      676  ---WM-----CRKORAGVMLVGTAKPDGSDPERMCRPYDE 708
Db      609  PRCLMPFRSGICGREYGLG-----DRWLELYJED 635

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RESULT 3
 T33026
 hypothetical protein T09A12.3 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
 C:Accession: T33026
 R:Hawkins, J.; Fulton, B.; Gillam, B.
 submitted to the EMBL Data Library, February 1998
 A:Description: The sequence of *C. elegans* cosmid T09A12.
 A:Reference number: Z21265
 A:Accession: T33026
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-900 <HAM>
 A:Cross-references: EMBL:AF047660; PIDD:AA004431.1; GSPDB:GN00022; CESP:T09A12.3
 A:Experimental source: strain Bristol N2; clone T09A12
 C:Genetics:
 A:Gene: CESP:T09A12.3
 A:Map position: 4
 A:Introns: 43/; 86/3; 260/2; 396/3; 424/2; 495/1; 517/3; 553/3; 691/3; 741/3; 780/3;

[illegible]

QY 376 LNKLOAKMDLLIRK-FFLNFCLMLTYMFTTAV-----AYHOP-- 413
 Db 409 LDTLLEAKWEAFARKNMIVSFATFLTYICVTAFTLRPIGFSTEMLTGWINRYSEBFP 468
 QY 414 -----FLKKAAP-----HKAQVSGMMLTGHIILLGIGIYLLV 448
 Db 469 GRYKNSSTQOVKPVINNTSGVLWSEPPLSQCHLRNWPDPIDPANSYIRLVEELEFVI 528
 QY 449 GOLYFMRHFFWIFISFD-----SYFELLFFQALLT-----VSOVLCELAIEW 494
 Db 529 GIC-----VQVFLDRFDRIKIRKKMMNVLTAFPAKITFKLYFLVLAIMPRLACL 581
 QY 495 YLPLLY-----SALVGLMNLTYTRGEQHTGISVMIOKVILRLDLRLIYLVFLF 547
 Db 582 SPVLVVDNVLITVMTFTFVHYLYGCVIRFVGPFLVMTYTIATDIFREMLIYGIFLM 641
 QY 548 GF--AVLVLSLSOAMRPEARTGPNATESVQPMGQDE-----GNGQX 590
 Db 642 GFSQSFSLIFLSCF--RANVYIKRLITDQSEASGSDKNKLNLTROI SAYDTAIVKMAEVF 699
 QY 591 RGLDEASLELF--KFTIGMELAFQEOLEFRGMVL-----LTLAYVLLTYILL 637
 Db 700 ENVMQSPLEAVRFTFLITGEFT----VLYRNALCPANFMWIGKVYFILFELFVSLMQ 755
 QY 638 LNMILALMSETVNSVATDSMSIMKLOKAISYLEME 672
 Db 756 FNMILAMTFTYETIFOTOLE-YKRORAOVILMLE 789

RESULT 4

T20312
 hypothetical protein F28H7.10 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
 C:Accession: T20312; T21533
 R:Matthews, P.
 Submitted to the EMBL Data Library, June 1996
 A:Accession number: Z19255
 A:Accession: T20312
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-790 <WIL>
 A:Cross-references: EMBL:Z74030; PIDN:CAA98449.1; GSPDB:GN00023; CESP:F28H7.10
 A:Experimental source: clone D1054
 R:Berts, M.
 Submitted to the EMBL Data Library, May 1996
 A:Reference number: Z19435
 A:Accession: T21533
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-790 <W12>
 A:Cross-references: EMBL:Z72508; PIDN:CAA96644.1; GSPDB:GN00023; CESP:F28H7.10
 A:Experimental source: clone F28H7
 C:Genetics:
 A:Gene: CESP:F28H7.10
 A:Map position: 5
 A:Introns: 46/2; 89/3; 129/1; 157/1; 201/1; 264/2; 349/3; 406/3; 487/3; 543/2; 580/1; 67

Query Match 9.8%; Score 392.5; DB 2; Length 790;
 Best Local Similarity 25.3%; Pred. No. 2.6e-22;
 Matches 182; Conservative 106; Mismatches 243; Indels 189; Gaps 35;
 QY 61 RKGGASQPD-PNRPDDRLEFNNAVSRGVEDLAGLPELSTKSYL-----TDSYXT 111
 Db 101 KKGKSGPNLIDFDDGO-----AEMAG--DLKALKLLDGGGKSGKSESYR 147
 QY 112 E-----GSTGKT-----CLMK--AVLNKLDGVNACILPLQIDRDSGNQP--LVNAQC 156
 Db 148 EWMVSVDERGSMGMLAICLGGSAHLNL-----IARRLINFPLINDIC 194
 QY 157 TDDYRGHSALHIAIEKRSLOQCVKLIVENGANVARACGRFF-----OKGQCT----- 204

Db 195 VSEYEGSLPHLAIIVNDOAFTSLRLGLADNORCYGAFPCADDOKASTDSEHEFV 254
 QY 205 -----CFYFGEPLSLSLACTKQMDVSYLLENPHOPASLOATDSOGNTVHALVM 254
 Db 255 ELTKNTNTGSMYGEYPLSFAICMGQHDLRMLLA---KANLSAQTNTNTALH-LCV 310
 QY 255 ISDNSAENIALVTSMYDGLLOAGARLCPTVOLIEDIRNLODLPKLAAK-EGKIEIFRH 313
 Db 311 IHDK-----MMLDVALEAGNI-----RLANKQNTALTALAKRKTESIOHL 355
 QY 314 LQREFSGLSH--LSRKTFEW--CYGPRVRSYLDIASVDCSENSVLEIAFNC----- 362
 Db 356 --ELMDGLIEQILDEK--WKAYG-----RALMURSLIGFTFFCCVCVAYML 398
 QY 363 -----KSPHRIRMYV-----LEPLNKLOAKMDLLIPKFLNFCNLIMFTFAVAHQ 412
 Db 399 RPSATTEHLTRGRINDGETESTNSTYLOMHA-----IDTOCHLMY--YSAWPYH 449
 QY 413 PTLKQAAPHKAEVNSMMLTGHIILLGIGIYLLVGOLMYFRRHWFIVISFDISFEI 472
 Db 450 GWMF-----LGCEIMTIYVLMFOILLDFGDIRRIGFQKWF-----NFLKAPPAK 493
 QY 473 LFLQALITVVSQVLCFLAI---EMYL-----PLVASVILGMLNLYTRRGFQHTGISV 525
 Db 494 LMFKAFLFIITISIPCRACSFHEFFLITDNTMAIISILTYQHFLYMRAPFVGPFLV 553
 QY 526 MIOKVILDLRLIYLVFLFEGAVALVSLSOAMRPEARTGPNATESVQPMGQDEG 585
 Db 554 MYTITATDVRFAMITYSIFLVGSQSFYLIFTSCERDS-----TAKKIDPM----- 601
 QY 586 NGAQYRGILE-----ASLEFKFTIGMELAFQE-----QLHFRGMVLLLLAYVLLYIL 636
 Db 602 -GSEFNINMEHPVDALLFTFIMTIGEFSLVREMSACDNFMKMIKLIIFVIFEFVSL 660
 QY 637 LNMILALMSETVNSVATDSMSIMKLOKAISYLEMENYMKCRKQKRGVNLVGTAPDG 696
 Db 661 QFNLLIAMTFTYETIFL-TRKEWKQWAOVILMLEMGLSPASRMH---LRLYTRPTG 715

RESULT 5

T37241
 olfactory channel protein osm-9 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
 C:Accession: T37241
 R:Colbert, H.A.; Smith, P.L.; Bargmann, C.I.
 J. Neurosci. 17, 8259-8269, 1997
 A:Title: OSM-9, A novel protein with structural similarity to channels, is required f
 A:Reference number: Z21639; MUID:97477445
 A:Accession: T37241
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-937 <COL>
 A:Cross-references: EMBL:AF031408; NID:g2642589; PIDN:AA887064.1; PID:g2642590
 C:Genetics:
 A:Gene: osm-9
 A:Map position: IV
 C:Keywords: transmembrane protein

Query Match 9.1%; Score 364; DB 2; Length 937;
 Best Local Similarity 23.9%; Pred. No. 5.4e-20;
 Matches 160; Conservative 101; Mismatches 254; Indels 154; Gaps 23;
 QY 98 LSKTSKYLITSEYTE-----GSTGKTCLMKAVLNKLDGVNACILPLQIDRDSGN 147
 Db 103 LSESVDMQOSRFRKHEVALMKLNKRGVGEN-LIHLNRPQOVCYETARLL-LKRPFG- 159
 QY 148 PQPLVNAQCTDDYRGSALHIAIEKRSLOQCVKLIVENGANVARACGRFF----- 198
 Db 160 ---MANDIYLADBOFGOSALHIAIVHDDYETVSLLSKADYVNRACGNFLPDPFKLTN 216
 QY 199 --OKGQCTCFYFGEPLSLSLACTKQMDVSYLLENPHOPASLOATDSOGNTVHALVMIS 256

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Db      217 KITDYOGGA-YGGGYPLAFPAACGNDIYDLLOFGANP-NLO--DSFGNTLHMCV----- 269
Qy      257 DNSAENIALTYSMYDGLLOAGARLCPTVQLEDIRNLQDTLPKLAAKEGIETIFRHILOR 316
Db      270 -----IYYSSMSYSVAVRHMAKPAD----PHYVNHAAGFTPLATLKRGKOIFEEMLE- 318
Qy      317 EFSGLSHSRFTEWCGYPRVSLYDASVDOE-----ENSVELIAFAHCSPHRR 369
Db      319 -----IMXVEFRPSDMTCSAVPPLNTLDTIOPDGSTNYDSALMTVI--NGSPEHLHD 368
Qy      370 MVYLEPRLNKLLQAOKMDLLIRKFELNFCNLIVMFI-FTAVAYHQPIKLQOAPPHIAEYG 428
Db      369 MIGSEVIQRIADKKAKFAQRKIIEERVLIIYQLITLSIYVYIRP---ELPRLYMEDP 424
Qy      429 NSMLLTGHILLLOGIYLIVGOLMYFKRVRVFWISEFIDSYPEILEFPALLTY----- 482
Db      425 Q-----WDYIIRTACELTILINCIFEFVGYOOLG 452
Qy      483 -----VSOVLCFLAIENVL-----PLAVSLAVIGLML 510
Db      453 EIROQGARGYLRANKTAPAKAVPCIALULPLLIOIPRLMKKHIEBALVYPALPGSWITL 512
Qy      511 LYTRGFQFHGTISVMYIQKVILRDLLRELLIYLVLEFGAVA--LYVLSQEAAMRPBAPTG 568
Db      513 LEPFARSAKLTPEFOYOTISMAGIMIFAISAIPLVFSQVPEFYGKMIDAKOKLEDTN 572
Qy      569 PNATESVOPMEGQODEBGANGVRSILIASLELFKPIITMGELAFQOGLHPFRGVLLLLLA 628
Db      573 PHACH-----TSGY-----TYTTINTFPEPTFTTLERASGGIDYEESCANAOALTITLEVL 624
Qy      629 YVLLTTYILLNMILALNSETVSNVAADSDWSIMKLORA--ISVLEMENGYNMCRCROKQAV 686
Db      625 YMFMPIIMIMIIILIAMGNNTYTIVYAQAEKAWMOQYAOIYMWLERSVG-----KERLAAS 679
Qy      687 MLTWGTRKD 695
Db      680 QLEYSTRID 688

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RESULT      6
T24772
hypothetical protein T10B10.7 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T24772
R:Sims, M.
submitted to the EMBL Data Library, May 1996
A:Reference number: Z19934
A:Accession: T24772
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-519 <MIL>
A:Cross-references: PIDN:CAA96679.1; CSPDB:GN00028; CESP:T10B10.7
A:Experimental source: clone T10B10
C:Genetics:
A:Gene: CESP:T10B10.7
A:Map position: X
A:Introns: 47/3; 139/1; 183/1; 215/2; 249/2; 385/3; 440/3

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Query Match	6.5%	Score 261;	DB 2;	Length 519;
Best Local Similarity	31.28;	Pred. No. 2.4e-12;		
Matches 90;	Conservative 32;	Mismatches 96;	Indels 70;	Gaps 12

QY	157	178	QY	205	238
TDYYR--GHSALHIALEKRSLOCVKLLVENGAVHWRACRFP-----OKSGG----	SEERYASGVSLPQALINEDLEWVYFLCRKGADVHRCYSFFCADDQKRSRDSLEHE	233	-----CFFGGLPLSLAACRKQMP-----VSTLLENPHQPSLQATDSQGNIVL	245	WVDLVSTKTYTGOMTGWGTYPLSPFACQATNOVDFRLRLRMKRDADPMP-----DINGSNIVL
204	233	291	245	291	

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QY 250 HALWISDMSNAENALYTSMDGLLOAGARCPYVQEDIRNODLTPLKLAKEGTEI 309
      .      :      :      :      :      :      :      :      :      :
Db 292 H-LTVIH-----LPEMTAVEIGANI-----HRRNMKLTPLALARLAKHI 335
QY 310 FRHILQREFSGLSHSRKFEWCYGPRLVSLYDLASVDSCB-----NSVLEITAFHC 362
      :      :      :      :      :      :      :      :      :
Db 336 YDLILECDMD-----ISWRGPPVCKAYPLINDVDTINESDGLSNPVSIAVAVYGD 386
QY 363 KSPHRHRMIVLEPLNKLOAKMDLLIKREFLNFNCNLTYMEIFTAAY 410
      :      :      :      :      :      :      :      :      :
Db 367 KYVDHLEFPDGL--IEEVLSEKWEFFGKOLPMSTAGTY--FLAVFY 429

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RESULT 7
119552
hypothetical protein C29E6.2 - *Caenorhabditis elegans*
C1:Species: *Caenorhabditis elegans*
C1:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C1:Accession: T19552
R1:Dobson, R.
submitted to the EMBL Data Library, May 1996
A1:Reference number: Z19141
A1:Accession: T19552
A1:Status: preliminary; translated from GB/EMBL/DBD1
A1:Molecule type: DNA
A1:Residues: 1-1188 <MIL>
A1:Cross-references: EMBL:Z72504; PIDN:CAA96603.1; GSPDB:GN00022; CESP:C29E6.2
A1:Experimental source: clone C29E6
C1:Genetics:
A1:Gene: CESP:C29E6.2
A1:Map position: 4
A1:introns: 147/2; 473/3; 500/1; 529/1; 584/2; 688/2; 839/3; 975/3; 1132/3

Query Match	5.2%;	Score 209;	DB 2;	Length 1188;
Best Local Similarity	19.1%;	Pred. No. 8.1e-08;		
Matches 152;	Conservative 110;	Mismatches 242;	Indels 290;	Gaps 39

[illegible]

QY 488 CF-----IAIEVYLLPLVLSALVGLWLNLYYRGQHTGIYSVMIOKVLRLDLRFLLLYL 543
 Db 900 CSATSGVQNMOMWILALACIFEEGMNLLFMIRKMRFCIFVMEVDIV-KTEFFRPFVAV 958
 QY 544 VFLGFAVALVLSLOEAMRPAPT---GPNATSEVQPMGEDEGNGAOYIGLEASLEL 600
 Db 959 LFIITAFSSSEFVILQN--RPEFTSTEMSPKLTVM--MIGE----- 995
 QY 601 FKFTIGMCELAFOELHFRGM-----VLLLLAYVLLTYLLLNLLALMSETVNSV 652
 Db 996 FEFT---GIFGDETHAEKKEFGPAHTAVACALFFFCIWTILMLLVGLAVDDINGV 1052
 QY 653 ATDSMSIWKLOKALS-VLEME-----NGY--WMCRRK 681
 Db 1053 -QEKAEELKRLAMQVDLYVQIBASLHFIOPTKKYATCRATPEPYGKLKTEFAGMWSNR 1111
 QY 682 QKAGVMTVGTRPD 695
 Db 1112 RRFG--LSVSTDPE 1123

RESULT 8
 JH0588
 Calmodulin-binding protein trpl - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 24-Sep-1998
 C:Accession: JH0588
 R:Phillips, A.M.; Bull, A.; Kelly, L.E.
 Neuron 8, 631-642, 1992
 A:Title: Identification of a Drosophila gene encoding a calmodulin-binding protein with
 A:Reference number: JH0588; MUID:92232293
 A:Accession: JH0588
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-1124 <PHI>
 A:Cross-references: GB:M88185; NID:g469057; PID:g158715
 A:Experimental source: head
 C:Genetics:
 A:Gene: trpl
 A:Cross-references: FlyBase:FBgn0005614
 C:Keywords: calmodulin binding; phosphoprotein; transmembrane protein
 F:341-362/Domain: transmembrane #status predicted <TM>
 F:374-396/Domain: transmembrane #status predicted <TM>
 F:462-479/Domain: transmembrane #status predicted <TM>
 F:512-533/Domain: transmembrane #status predicted <TM>
 F:549-572/Domain: transmembrane #status predicted <TM>
 F:643-668/Domain: transmembrane #status predicted <TM>
 F:710-727/809-825/Region: calmodulin binding #status predicted
 F:722/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 4.9% Score 197.5; DB 2; Length 1124;
 Best Local Similarity 19.7% Pred. No. 5.0e-07;
 Matches 167; Conservative 130; Mismatches 281; Indels 249; Gaps 38;
 QY 131 VNACILPLQLDRDSGNPOLP-----VNAQCTDD 159
 Db 25 VGGCCVPL-----GLPQLLEKKFLAVERGDMNVRRILQKALRHQHNINCMRP 77
 QY 160 YRSHSLAHIAIEKRSLQCVKLVENG-----ANVHARAC-----GRFQKG 201
 Db 78 L--GRRALTLADINENLEWELLVMGVETKDALHAINAEFVAVELLEHEELIYKEG 135
 QY 202 Q-----GTCEYFGEL-PLSLACGKKMDVSYLLEN-----PH-----QPSAL 238
 Db 136 EPIYMWQVDITAMFAFDITPLMLAAHKNNFEILRLDRGAAPVPRHDICGCEBCVRL 195
 QY 239 QATDSQNTVLH-----ALVMSDSNAENIALVTSMYDILQAGARLCPTVOLED 288
 Db 196 TAEDSLRLHSLSRVNIYALCSPSLICLTSSNDPSSATPQLSMLNIALTEBECKSEYMDL 255
 QY 289 IRNLQ-----DLTPKLAKBEGKIEL-----FRHILQREPSGLSHLSKRTYEW 332

Db 256 RRQCKFAVDLLDQTRTSNEALIIILNDPQMSSEYEPGRMSLTRYQAISYKOKFV--A 313
 QY 333 YGPVRSVLS-----YDLASVDSCEBNSVLEIIAFHCKSPRHRRNVLEPINKLL-----QAK 383
 Db 314 HSNIOQLLSIWD--GLPGRKRSIVDKV--CIA-----QVAVLPFLYCLILMCAPR 365
 QY 384 WDLIPKPFELNLCN-----LIYMEFTVA-----YHOPTLKQAAPHKAEVGN 429
 Db 366 TGOIMRKPFMFLHASSYLFLLILVLSQRADDPFRIGTPTMKKLEBOELRQGO 425
 QY 430 SMLTGHLILILGTYLLVQGLMYFRNRHFIWISFIDSYEILFLQALL--TVSQYL 487
 Db 426 ----TPSKLELIVMYV----IGFVMEVQEIFAVGMSYLRNMNFIDFLRNSLYVSV 477
 QY 488 CELAIEM-----YLP-----LLVSLVLGWLMLLYTTREFQ 518
 Db 478 CLRAFAITQATEIARDPOMATIPREKWHDPDOLIAGLFAAANVSALVHLFSTNP 537
 QY 519 HTGIYSVMIOKVLRLDLRFLLYLVLEFGAVALVLSQEAW-----REAPTPGNAT 572
 Db 538 HGLPQLISLGRNVI-DYKFFFTIVLFAPA---CGNLQMLMFAALEKSKCYLPG-- 591
 QY 573 ESVQPMGEDEGNGA-----QYIGLEASLELFKFTIGMEL-----AFQDLHFR 619
 Db 592 -----GEADMGSHGDCMKMRFRGNLFESSOSLFMASFGMGVGLDFELSGIKSYTRFW 644
 QY 620 GMVLLLLAYVLLTYLLLNLLALMSETVNSVATDSISIKLOKALSIVLEMENGYWCR 679
 Db 645 G--LIMFSGYSVINIVTLNLLIMMSNSYAMIDEHSDTEWKFPAK-----TKLMSY 694
 QY 680 KQKAGVMTVGTRPDGSPDERMCFRV-----EEVMAWMEOTLPTLC 722
 Db 695 FEDSA-----TLPPFNVLPSVKWYIRIFRKSCKTIDROSKRKREQBEFSYDINIRSLV 750
 QY 723 EDPGAGVPTLENVLASPKEDD--DGASENVVPVQLIQ 762
 Db 751 W-RYVAAMHRRFEN---NPVSEDDINEVKSEINMYREMLE 787

RESULT 9
 JN0015
 trp protein - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 02-Feb-2001
 C:Accession: JN0015
 R:Wong, F.F.; Schaefer, E.L.; Roop, B.C.; Lamendola, J.N.; Johnson-Seaton, D.; Shao, D.
 Neuron 3, 81-94, 1989
 A:Title: Proper function of the Drosophila trp gene product during pupal development
 A:Reference number: JN0015; MUID:90148782
 A:Accession: JN0015
 A:Molecule type: mRNA
 A:Residues: 1-1274 <WON>
 C:Comment: This photoreceptor membrane-associated protein is not required for the occ
 C:Genetics:
 A:Gene: trp
 A:Cross-references: FlyBase:FBgn0003861
 A:Map position: 99C5-6
 C:Superfamily: TRPC3 protein
 C:Keywords: glycoprotein; nucleotide binding; P-loop; phosphoprotein; transmembrane P
 F:1257-1263/Region: nucleotide-binding motif A (P-loop)
 F:164,70,899/Binding site: carbohydrate (asn) (covalent) #status predicted
 F:191,602,880,883,924/Binding site: phosphate (Ser) (covalent) #status predicted
 F:800,1266/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 4.8% Score 191; DB 2; Length 1274;
 Best Local Similarity 20.2% Pred. No. 2.2e-06;
 Matches 134; Conservative 99; Mismatches 237; Indels 192; Gaps 30;
 QY 153 NAOCTDYYRSHSLAHIAIEKRSLQCVKLVLENGANVHARACGRFQKGGCTCYFFGLP 212
 Db 62 NINCTDPNMR--SALISAIEENENFDLWILLEHNEY-----GDALLHAISEEY 108


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OY 86 GVPEDLAGLPEY-----LSKTSKYITDSEYTBGSGTKCTLMKAV----- 124
    |||
    |||
Db 37 GAPPSPGLPSPMAAMAAALPSTDLGASSSSLPSSPSSSPNEVMALKDQVREKEENT 96
OY 125 LNLKGVNAC-----ILPLLOIDROSGNPQPLVNAOCTDDYRGSAHIAIEKRSIQ 177
    |||
    |||
Db 97 LNEKLFPLACCKGDIYWKLE--ENSSGD--LNLNCVD--VLGRAAVITTEENELD 149
OY 178 CVKLLVENGAVNARACGRFQKGTGCF--YFGEPLSLAACKOMDVSYLLE----- 230
    |||
    |||
Db 150 ILQOLLIDYG-----COKLMERIQNPESYTTMDVAPVILAHNNNYELLMLKQDVSL 202
OY 231 -NPH-----OPASLOATDSOGNTVLHMLVMSD 257
    |||
    |||
Db 203 PKPAVACECTLSAKKKKDSLRSRFLDIYRCLASPALIMTEE--DPILRAFELSD 260
OY 258 -----NSAENIALVTSWYDGLQAGARLCPTVOEDIRN----- 291
    |||
    |||
Db 261 LKELSLVEVERNDYEEELARCKMFAKDLAQAR--NSRELEVILNMTSSDEPLDKRGL 318
OY 292 --LQDLPLKLAKEGKIEIFRHILQREFSGLSHSRKFTMCYGPVAVSLYDLASVDS 349
    |||
    |||
Db 319 EERNLISRLKALIKYN-----QKEF-----VSQSN 344
OY 350 EENSVELIAPHCSPHRHR-----MYLE-----PLNKL-----QAKDILLPKFEL 393
    |||
    |||
Db 345 QO--FLMTVMFGOMSGYRRKPTCKIMTVLGIFWPLSLICYLIAPKSGRIIHPFM 402
OY 394 NELCNLIYMEFT-----ANAYHOPILKQAARPKAEVNSMLTGILLGCIYLL 447
    |||
    |||
Db 403 KFTIHGASYFFLLILNLISLVNEDK-----KNTMGPALERIDYLL-----WT 448
OY 448 VQGLMFWRRHVFIMISFIDSYFE-----ILFLQA--LLTVNSQVLCFLAI-----E 493
    |||
    |||
Db 449 IGMIMSDIKR--LMYGLIEDFLESRNQSLFVNNSLYLAFALKVYAHNNKHFADKRD 505
OY 494 W--VLPLVSAVLVGMNLVYTRGFOHTGYSVM-----IQKYLKDLPLLIYVEL 546
    |||
    |||
Db 506 WDAHPPLVLAAGLFAFANVLYLRLFFMYTTSILGPLQISMGMLODFGLMFLIYL 565
OY 547 FGFVALVLSQGEAMREPAPGPNATESVQPMGEODEGNAOYRGILAELELFKPTIG 606
    |||
    |||
Db 566 FSFITGLTQLYDKGY-----TSKQKDCVGIFFCQOSNDT---FHSFGTCFALFWYFS 617
OY 607 MGEIATF-----QEOLHFRGMVLLLLAVLLTYILLMLTALMSETVNSVATDSWS 658
    |||
    |||
Db 618 LAHVAIFVTRSYGEBLQSFVGAIV--IVGTYNVVIVITLTLVLAAMLHKSQOLLANHEDK 675
OY 659 IWKLQKA 665
    |||
    |||
Db 676 EMKFAFA 682

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RESULT 12
 H71274
 Probable ankryrin - syphilis spirochete
 C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: H71274
 R:Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin
 rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Uterback, T.; McD
 they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
 Science 281, 375-388, 1998
 A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
 A:Reference number: A71250; MUID:9832770
 A:Accession: H71274
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-934 <COL>
 A:Cross-references: GB:AE001254; GB:AE000520; NID:9323148; PIDN:AAC65803.1; PID:93232314
 A:Experimental source: strain Nichols
 C:Genetics:
 A:Gene: TP0835

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C:Superfamily: syphilis spirochete probable ankryrin; ankryrin repeat homology  

F:281-313/Domain: ankryrin repeat homology <AN22>

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Query Match 4.28; Score 167.5; DB 1; Length 934;
 Best Local Similarity 27.68; Pred. No. 9.7e-05;
 Matches 72; Conservative 37; Mismatches 95; Indels 57; Gaps 10;

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OY 76 RDRLEFNASRVPEDLAGLPEYLSKTSKYITDSEYTBGSGTKCTLMKAVL----- 126
    |||
    |||
Db 448 RDLPLHAVASRAHNDIV---KELFRERQW---IARDTKMTILHVAVANDDAVAGEFL 500
OY 127 LKQGVNAC-----ILPLLOIDROSGNPQPLVNAOCTDDYRGSAHIAIEKR 174
    |||
    |||
Db 501 MREGADIFSTWVHVSPLKLTATTSGRREDWILTAANYHAODTG--GNPLHLACEMK 556
OY 175 SLOCVLLVENGAVNARACGRFQKGTGCFYFGEPLSLAACKOMDVSYLLE-NPH 233
    |||
    |||
Db 557 LQQAINGILRRGAETEARNLQ-----ETPLFSAVSDAEVISILHPQAG 603
OY 234 QPASLOATDSOGNTVLHMLVMSDNSAENIALVTSWYDGLQAGARLCPTVOEDIRNLQ 293
    |||
    |||
Db 604 NPALVDARDAGNTVLAHCVRMSALRSADVL-----IREADAR---HVSILNARLIS 652
OY 294 DLPLKLAKEGKIEIFRHIL 314
    |||
    |||
Db 653 GKPLHLAARAGNVDFIRLL 673

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RESULT 13
 T23729
 hypothetical protein M05B5.6 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T23729
 R:Gardner, A.
 Submitted to the EMBL Data Library, April 1996
 A:Reference number: Z19790
 A:Accession: T23729
 A:Molecule type: translated from GB/EMBL/DBJ
 A:Status: preliminary;
 A:Residues: 1-481 <WIL>
 A:Cross-references: EMBL:Z19790; PIDN:CAA95836.1; GSPDB:GN00019; CESP:M05B5.6
 A:Experimental source: clone M05B5
 C:Genetics:
 A:Gene: CESP:M05B5.6
 A:Map position: 1
 A:introns: 50/2; 99/1; 133/3; 185/3; 229/3; 402/3; 457/3

Query Match 3.9%; Score 157.5; DB 2; Length 481;
 Best Local Similarity 23.08; Pred. No. 0.00024;
 Matches 90; Conservative 58; Mismatches 149; Indels 95; Gaps 17;

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OY 291 NLQDLTPKLAKEGKIEIFRHILQREFSGLSHSRKFTMCYGPVAVSLYDLASVDSCE 350
    |||
    |||
Db 57 NMEKRLKLSGKKWG---VIRH-----PYLNVVNOKLIDCAFFYS-- 94
OY 351 ENSVLEIAPHCSPHRHNVLEPINKLQAKDILLPKFELNLCILYMFETAVAY 410
    |||
    |||
Db 95 ---LHILAF-----LVFLLAHMVSRNLKFDPL---TTFGTGIF 130
OY 411 HQPLKQAARPKAEVNSMLTGILLGCIYLLVQGLMFWRRHVFIMISFIDSYF 470
    |||
    |||
Db 131 MFLVLKGF---IKARITKS-VSTWFIYAFQCNIFTYMATLAVYWLPTVF---GYDDVHL 182
OY 471 EILFLQALLTVNSQVLCFLAIEWYLPPLVSAVLVGMNLVYTRGFOHTGYSVMTOKV 530
    |||
    |||
Db 183 EVKRI-----VTWFLPPI--AIIASAMNLIIYIMRK--SPFGIYIFMMTR- 222
OY 531 ILRDLRLFLIYLVFLGFAVALVLSQGEAMREPAPGPNATES---VQPMGEDEGNG 587
    |||
    |||
Db 223 ILRSFAHIAITWPLTAFSAFLIMRDGVKFWPLIDQOTEMTMVQTM----- 273

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